

GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: March 16, 2005, 21:10:15 ; Search time 147.538 Seconds
(without alignment)
1436.539 Million cell updates/sec

Title: US-10-017-168-20

Perfect score: 2796
Sequence: 1 MFVSDMPKQYAVRISNLE.....AVLENFQRFKADFLKAR 548

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A: Geneseq_16Dec04:*
1: geneseqp1808:*
2: geneseqp1908:*
3: geneseqp2008:*
4: geneseqp20018:*
5: geneseqp20038:*
6: geneseqp20038:*
7: geneseqp20038:*
8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2178	77.9	432	4	AA848316
2	1479	52.9	312	4	AA848318
3	1043	37.3	232	4	AA848317
4	280	10.0	2768	4	AB868397
5	271	9.7	783	2	AA05804
6	269	9.6	567	4	AA813147
7	268.5	9.6	1000	6	ABU25647
8	259	9.3	522	4	AAE02397
9	257	9.2	412	2	AAW03626
10	250	8.9	902	4	AA829778
11	250	8.9	1018	2	AA898747
12	250	8.9	1018	2	AAW97039
13	250	8.9	1018	2	AA866528
14	250	8.9	1018	8	ADJ95471
15	243	8.7	360	2	AAW03627
16	242	8.7	34350	8	ADQ89964
17	236.5	8.5	2109	8	ADN23693
18	232.5	8.3	552	7	ADN31182
19	228	8.2	1388	6	ABJ38696
20	226	8.1	553	7	ADW05820
21	224	8.0	1388	7	ADJ69333
22	223	8.0	489	4	AB858655
23	223	8.0	485	6	ABW04814
24	222	7.9	864	4	AAW39026
25	220.5	7.9	486	5	AAE23036

26	217	7.8	611	2	AAV29039
27	217	7.8	611	4	AAU25510
28	217	7.8	611	7	ADG17131
29	217	7.8	611	4	AB858691
30	216	7.7	1501	5	AAU76762
31	216	7.7	1568	6	ABP70152
32	213.5	7.6	382	4	AAE02399
33	213	7.6	4412	3	AAV53666
34	211	7.5	3551	8	ADQ01006
35	210	7.5	1192	4	AB858642
36	210	7.5	1965	8	ADK47314
37	210	7.5	1972	8	ADR94616
38	208.5	7.5	293	4	AAE02398
39	206.5	7.4	474	8	ADN46475
40	206	7.4	869	7	AD160170
41	205	7.3	385	6	ABU20070
42	204	7.3	1026	4	AAW78825
43	203	7.3	1245	6	ABP56885
44	203	7.3	2397	6	ABU43308
45	201	7.2	897	4	AAU37176

ALIGNMENTS

RESULT 1	AA848316	standard; protein; 432 AA.
XX	XX	
XX	AA848316;	
AC	XX	
XX	11-SEP-2003 (revised)	
DT	20-APR-2001 (first entry)	
XX	XX	
DE	T. pallidum ssp. pallidum (N1) acidic repeat protein (arp).	
XX	XX	
KW	Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis;	
XX	Yaws; bejel.	
OS	Treponema pallidum; ssp. pallidum.	
XX	XX	
PN	MO200077486-A2.	
XX	XX	
PD	21-DEC-2000.	
XX	XX	
PF	14-JUN-2000; 2000WC-US016425.	
XX	XX	
PR	14-JUN-1999; 99US-0138981P.	
XX	XX	
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.	
XX	XX	
PI	Liu H, Steiner B, Rhodes B;	
XX	XX	
DR	WPI; 2001-080711/09.	
XX	XX	
DR	N-PSDB; AAC84647.	
PT	Detecting Treponema pallidum in blood, saliva, etc., by detecting	
PT	formation of a complex between immunogenic peptides of acidic repeat	
PT	protein of the bacterium and an antibody present in the biological	
PT	sample.	
XX	XX	
PS	Claim 15; Fig 6; 73pp; English.	
XX	XX	
CC	The invention relates to a method of detecting presence of Treponema	
CC	pallidum (Tp), anti-treponemal antibodies (Abs) or both in a biological	
CC	sample that involves contacting an acidic repeat protein (arp) or one or	
CC	more isolated immunogenic TP peptides of arp with an Ab containing	
CC	biological sample and then detecting the formation of a complex between	
CC	immunogenic peptides and Ab. The presence of the complex indicates the	
CC	presence of TP. The method is thus useful for diagnosing syphilis, yaws,	
CC	and bejel diseases. The immunogenic peptides or the Abs raised against	
CC	arp, as part of an immunogenic composition, are useful for inducing a	
CC	protective immune response against syphilis, yaws or bejel caused by TP.	
CC	AAV29039 T. gondii	
CC	AAU25510 T. gondii	
CC	ADG17131 T. gondii	
CC	AB858691 Drosophila	
CC	AAU76762 Plasmodium	
CC	ABP70152 Anisakis	
CC	AAE02399 Canine re	
CC	AAV53666 Sequence	
CC	ADQ01006 Mouse hom	
CC	AB858642 Drosophila	
CC	ADK47314 Streptococcus	
CC	ADR94616 Novel S.	
CC	AAE02398 Canine re	
CC	ADN46475 Thermococcus	
CC	AD160170 Secreted	
CC	ABU20070 Protein e	
CC	AAW78825 Human pro	
CC	ABP56885 Staphylococcus	
CC	ABU43308 Protein e	
CC	AAU37176 Staphylococcus	

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OM protein - protein search, using sw model

Run on: March 16, 2005, 21:14:51 ; Search time 31.1136 Seconds
(without alignments)
1694.657 Million cell updates/sec

Title: US-10-017-168-20

Perfect score: 2796
Sequence: 1 MFRVSDMPFQNTAVEISNLE.....AVLENFQFGKDAFLKKAR 548

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: PIR 79:*

1: PIR1:*\n2: PIR2:*\n3: PIR3:*\n4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1091.5	39.0	227	2 G71326	hypothetical prote
2	967	34.6	256	2 F71326	hypothetical prote
3	290.5	10.4	1110	2 I51116	NF-180 - sea lamp
4	273	9.8	1271	2 A45555	glutamate rich pro
5	271.5	9.7	721	2 S29795	hypothetical prote
6	268.5	9.6	913	2 T52485	neurofilament prot
7	253	9.0	590	2 A40437	glutamic acid-rich
8	247	8.8	391	2 S27850	surface antigen TC
9	242	8.7	7962	2 I18346	elastic titin - hu
10	240	8.6	1094	2 S49313	protein kinase - s
11	236.5	8.5	2109	2 B89066	protein H05009.1 l
12	236.5	8.5	2109	2 T73247	hypothetical prote
13	236	8.4	407	1 EDBE03	hypothetical prote
14	227	8.1	1621	2 A82255	hypothetical prote
15	224.5	8.0	544	1 I13691	involucrin L - dou
16	224.5	8.0	630	2 S29796	hypothetical prote
17	223	8.0	845	2 A45669	neurofilament trip
18	221.5	7.9	1262	2 T72523	hypothetical prote
19	220.5	7.9	1560	2 T70282	calcium-binding pr
20	220	7.9	506	2 S47439	I2 protein - Trypa
21	219	7.8	679	2 S28366	recombination repa
22	216	7.7	849	2 S00030	neurofilament tri
23	213	7.6	296	2 A54527	110k antigen - pla
24	212	7.6	644	2 S55355	neurofilament prot
25	211	7.5	411	2 S47436	flagellar antigen
26	206	7.4	493	1 A57783	involucrin - cotto
27	201	7.2	6642	2 T29757	protein UNC-89 - C
28	200	7.2	1881	2 H95076	zinc metalloprotei
29	198.5	7.1	916	2 A27864	neurofilament trip

30	197	7.0	924	2 S27923	gene Lf3 protein -
31	197	7.0	1020	1 QFRU02	neurofilament trip
32	197	7.0	1563	2 B96002	Iga-specific metal
33	196.5	7.0	798	2 I50479	neurofilament medi
34	196.5	7.0	2722	2 T20532	hypothetical prote
35	196.5	7.0	2738	2 E88320	protein F07A11.6 l
36	196	7.0	387	2 D84885	hypothetical prote
37	195	7.0	754	2 AC2807	Ompa family protei
38	195	7.0	754	2 B97586	hypothetical prote
39	194.5	7.0	699	2 T01029	hypothetical prote
40	194	6.9	1300	2 T03166	probable immediate
41	192.5	6.9	2004	2 F95133	immunoglobulin Al
42	192	6.9	837	2 JN0292	antigen 332 - mala
43	191.5	6.8	1199	2 S20969	Na+/Ca2+-K+-exchan
44	191	6.8	5170	2 T15348	hypothetical prote
45	190.5	6.8	880	2 D89756	protein T23E7.2b l

ALIGNMENTS

RESULT 1

G71326 hypothetical protein TP0434 - syphilis spirochete

C/Species: Treponema pallidum subsp. pallidum (syphilis spirochete)

C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004

R/Frazer, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gw

erson, J.; Khatalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McI

they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.

Science 281, 375-388, 1998

A/Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.

A/Reference, number: A71250; M01D:9832270; PMID:9665876

A/Accession: G71326

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-227 <COL>

A/Cross-references: UNIPROT:083449; GB:AE001220; GB:AE000520; NID:93322705; PIDN:AC654

A/Experimental source: strain Nichols

C/Genetics:

A/Gene: TP0434

Query Match	39.0%	Score 1091.5;	DB 2;	Length 227;
Best Local Similarity	93.8%	Pred. No. 3.1e-52;		
Matches 213;	Conservative 2;	Mismatches 11;	Indels 1;	Gaps 1;
QY	322	REGGEREVDVPRVVEPASEREGREVEDVPRVVEPASEREGREVEDVPRVVEPASEG	381	
DB	2	REGSVR-WPTCRRYVEPASEREGREGGGLPRVVEPASEREGREVEDVPRVVEPASEG	60	
QY	382	HEGGEREVDVPRVVEPASEGREGREVEDVPRVVEPASEGREGREVEDVPRVVEPASEG	441	
DB	61	HEGGEREVDVPRVVEPASEGREGREVEDVPRVVEPASEGREGREVEDVPRVVEPASEG	120	
QY	442	DLSESEIIVPEBQKRAHPQVTPGAPRGLOPEYVVOJAVFDATQVOSIVHRYGVEXF	501	
DB	121	DLSESEIIVPEBQKRAHPQVTPGAPRGLOPEYVVOJAVFDATQVOSIVHRYGVEXF	180	
QY	502	IAVEDIHEGKVFQVCGPVQKDERGAVLENFQFGFQDAFLKKAR	548	
DB	181	IAVEDIHEGKVFQVCGPVQKDERGAVLENFQFGFQDAFLKKAR	227	

RESULT 2

F71326 hypothetical protein TP0433 - syphilis spirochete

C/Species: Treponema pallidum subsp. pallidum (syphilis spirochete)

C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004

C/Accession: F71326

R/Frazer, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gw

erson, J.; Khatalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McI

they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.

Science 281, 375-388, 1998

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OM protein - protein search, using sw model

Run on: March 16, 2005, 21:13:20 ; Search time 139.007 Seconds
(Without alignments)
2018.738 Million cell updates/sec

Title: US-10-017-168-20

Perfect score: 2796
Sequence: 1 MFVRSMPFKNTAVETISNLE.....AVLENFQRFKDAFLKKAR 548

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot_sprot.*
2: uniprot_tr embl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2796	100.0	548	2	Q93CA4
2	2178	77.9	432	2	Q51953
3	2092	74.8	428	2	Q9ALV6
4	1899.5	67.9	393	2	Q93CA3
5	1656	59.2	348	2	Q9ALV7
6	1091.5	39.0	227	2	Q83449
7	967	34.6	256	2	Q83448
8	536	19.2	458	2	Q73NG7
9	303.5	10.9	1112	2	Q63G96
10	301.5	10.8	1108	2	Q9ND10
11	296	10.6	5458	2	Q9U459
12	290.5	10.4	1110	2	Q91255
13	280	10.0	2768	2	Q9VC00
14	277.5	9.9	897	2	Q13098
15	273	9.8	1271	2	Q25860
16	271.5	9.7	721	1	YCF2_OENPI
17	271.5	9.7	1554	2	Q7RMX1
18	271	9.7	843	2	Q6GKMO
19	269	9.6	432	2	Q964C9
20	269	9.6	567	2	Q9HD28
21	269	9.6	3455	2	Q6R5A9
22	268.5	9.6	913	2	Q61309
23	268.5	9.6	913	2	Q6DCCO
24	265	9.5	982	2	Q73C08
25	261.5	9.4	1394	1	CNG4_BOVIN
26	259	9.3	572	2	Q8MKF9
27	259	9.3	1233	2	Q81U56
28	257	9.2	722	2	Q26893
29	256.5	9.2	248	2	Q9LRH2
30	256	9.2	466	2	Q6NE60
31	256	9.2	5507	2	Q81HN3

32	253.5	9.1	501	2	Q80BK7	Q80BK7
33	250.5	9.0	1167	2	Q7SH94	Q7SH94
34	249.5	8.9	501	2	Q80AG4	Q80AG4
35	249	8.9	791	2	Q9DGL1	Q9DGL1
36	248	8.9	1070	2	Q81YTO	Q81YTO
37	247	8.8	391	2	Q26892	Q26892
38	246.5	8.8	716	2	Q801T3	Q801T3
39	245.5	8.8	690	2	Q6PCS2	Q6PCS2
40	245.5	8.8	1236	2	Q9GTX2	Q9GTX2
41	244	8.7	3134	2	Q81414	Q81414
42	242	8.7	7962	2	Q10465	Q10465
43	242	8.7	34350	2	Q8WZ42	Q8WZ42
44	240	8.6	979	2	Q8T9Y2	Q8T9Y2
45	240	8.6	1094	2	Q23915	Q23915

ALIGNMENTS

Query Match	Score	DB 2	Length	548
Best local similarity	100.0%	Pred. No. 4.8e-129		
Matches	548	Conservative	0	Mismatches 0; Indels 0; Gaps 0;
QY	1	MFVRSMPFKNTAVETISNLEKAKAQAQVYIGAGIPLGLVSLAPLAAAGLGIVYQAVRV	60	
DB	1	MFVRSMPFKNTAVETISNLEKAKAQAQVYIGAGIPLGLVSLAPLAAAGLGIVYQAVRV	60	
QY	61	RVRTIGTVAGSOTSODGLSLASLPSPVAPAPORBDPLSSPPAGHTVPEYRDTVIFDDPR	120	
DB	61	RVRTIGTVAGSOTSODGLSLASLPSPVAPAPORBDPLSSPPAGHTVPEYRDTVIFDDPR	120	
QY	121	LVSPLSREVEDAPKVPSPASREGEEREVEDAPKVPSPASREGEEREVEDAPKVPSPAS	180	
DB	121	LVSPLSREVEDAPKVPSPASREGEEREVEDAPKVPSPASREGEEREVEDAPKVPSPAS	180	
QY	181	EBEGGEREVEDAPKVPSPASREGEEREVEDAPKVPSPASREGEEREVEDAPKVPSPAS	240	
DB	181	EBEGGEREVEDAPKVPSPASREGEEREVEDAPKVPSPASREGEEREVEDAPKVPSPAS	240	
QY	241	EBEGGEREVEDAPKVPSPASREGEEREVEDAPKVPSPASREGEEREVEDAPKVPSPAS	300	
DB	241	EBEGGEREVEDAPKVPSPASREGEEREVEDAPKVPSPASREGEEREVEDAPKVPSPAS	300	
QY	301	EBEGGEREVEDAPKVPSPASREGEEREVEDAPKVPSPASREGEEREVEDAPKVPSPAS	360	
DB	301	EBEGGEREVEDAPKVPSPASREGEEREVEDAPKVPSPASREGEEREVEDAPKVPSPAS	360	
QY	361	EBEGGEREVEDAPKVPSPASREGEEREVEDAPKVPSPASREGEEREVEDAPKVPSPAS	420	
DB	361	EBEGGEREVEDAPKVPSPASREGEEREVEDAPKVPSPASREGEEREVEDAPKVPSPAS	420	
QY	421	VNSAPNQRNPEGELFTLPDLSSEIIVPEOKRAHPQVTPICAPRGLQPGETYYQI	480	
DB	421	VNSAPNQRNPEGELFTLPDLSSEIIVPEOKRAHPQVTPICAPRGLQPGETYYQI	480	

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OM protein - protein search, using sw model

Run on: March 16, 2005, 21:10:15 ; Search time 84 Seconds

(without alignments)
1436.539 Million cell updates/sec

Title: US-10-017-168-6

Perfect score: 1572

Sequence: 1 MFVRSDFMFPKNTAVELISNLE.....HTKQPSHSVSNAPNCFRKP 312

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16dec04:*
1: geneseqp19808:*
2: geneseqp19908:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20048:*
8: geneseqp20058:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1572	100.0	312	4	AAB48318 T. pallid
2	1480	94.1	432	4	AAB48316 T. pallid
3	1118	71.1	232	4	AAB48317 T. pallid
4	214.5	13.6	1018	2	AAR98747 P. vivax
5	214.5	13.6	1018	2	AAR97039 A. secreta
6	214.5	13.6	1018	4	AA66528 Plasmodiu
7	214.5	13.6	1018	8	ADJ95471 Plasmodiu
8	187.5	11.9	2109	8	ADN23653 Bacteri
9	187.5	11.9	2109	8	ADN23653 Bacteri
10	183	11.6	783	4	AAR05804 Drosophila
11	179	11.4	552	7	ADC31182 Human nov
12	171	10.9	194	4	ABG11265 Human nov
13	167.5	10.7	1000	6	ABJ25647 Novel hum
14	159	10.1	258	2	AAW55107 Streptoco
15	159	10.1	258	2	AAW55107 Streptoco
16	159	10.1	258	2	AAW55107 Streptoco
17	159	10.1	258	2	AAW55107 Streptoco
18	159	10.1	258	2	AAW55107 Streptoco
19	159	10.1	258	2	AAW55107 Streptoco
20	159	10.1	258	2	AAW55107 Streptoco
21	159	10.1	258	2	AAW55107 Streptoco
22	159	10.1	258	2	AAW55107 Streptoco
23	159	10.1	258	2	AAW55107 Streptoco
24	159	10.1	258	2	AAW55107 Streptoco
25	156.5	10.0	522	4	AAB02397 Canine re

26	155.5	9.9	486	5	AAB23036 Human chi
27	155.5	9.9	1026	4	AAM78825 Human pro
28	155	9.9	197	6	ABP56385 Polyanion
29	155	9.9	198	6	ABP56380 Polyanion
30	154	9.8	181	6	ABP56382 Polyanion
31	154	9.8	186	6	ABP56381 Polyanion
32	154	9.8	187	6	ABP56384 Polyanion
33	154	9.8	360	2	AAW03627 Human fol
34	154	9.8	466	6	ABU20421 Human thy
35	153.5	9.8	412	2	AAW03626 Human thy
36	153.5	9.8	864	4	AAW03626 Human thy
37	153.5	9.8	1388	6	ABJ38696 Human nuc
38	153.5	9.8	1388	6	ABJ38696 Human nuc
39	153	9.7	1963	8	ADK48728 Streptoco
40	152.5	9.7	488	3	AAW42093 Human ORF
41	151.5	9.6	617	4	ABM16458 Peptide #
42	151.5	9.6	617	4	ABM16458 Peptide #
43	151.5	9.6	617	4	ABM16458 Peptide #
44	151.5	9.6	617	4	ABM16458 Peptide #
45	151.5	9.6	617	4	ABM16458 Peptide #

ALIGNMENTS

RESULT 1	AA048318	standard; protein; 312 AA.
XX	AA048318	
AC	AA048318	
XX	AA048318	
DT	11-SEP-2003 (revised)	
DT	20-APR-2001 (first entry)	
XX	T. pallidum ssp. endemicum (Bosnia) acidic repeat protein (arp).	
DE	T. pallidum ssp. endemicum (Bosnia) acidic repeat protein (arp).	
KW	Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis;	
XX	Yaws; bejel.	
XX	Treponema pallidum; ssp. endemicum.	
OS	WO200077486-A2.	
PN	WO200077486-A2.	
XX	21-DEC-2000.	
PD	14-JUN-2000; 2000MO-US016425.	
PF	14-JUN-2000; 2000MO-US016425.	
XX	14-JUN-1999; 99US-0138981P.	
PR	(USSH) US DEPT HEALTH & HUMAN SERVICES.	
XX	Liu H, Steiner B, Rhodes B;	
XX	WPI; 2001-080711/09.	
DR	N-Peptide; AAC84649.	
XX	Detecting Treponema pallidum in blood, saliva, etc., by detecting	
PT	formation of a complex between immunogenic peptides of acidic repeat	
PT	protein of the bacterium and an antibody present in the biological	
PT	sample.	
XX	Claim 15; Fig 10; 73pp; English.	
PS	The invention relates to a method of detecting presence of Treponema	
CC	pallidum (TP), anti-treponemal antibodies (Abs), or both in a biological	
CC	sample that involves contacting an acidic repeat protein (arp), or one or	
CC	more isolated immunogenic TP peptides of arp with an Ab containing	
CC	biological sample and then detecting the formation of a complex between	
CC	immunogenic peptides and Ab. The presence of the complex indicates the	
CC	presence of TP. The method is thus useful for diagnosing syphilis, yaws,	
CC	and bejel diseases. The immunogenic peptides or the Abs raised against	
CC	arp, as part of an immunogenic composition, are useful for inducing a	
CC	protective immune response against syphilis, yaws or bejel caused by TP.	

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OM protein - protein search, using sw model

Run on: March 16, 2005, 21:14:51 / Search time 17.7143 Seconds
(without alignment)
1694.657 Million cell updates/sec

Title: US-10-017-168-6

Perfect score: 1572

Sequence: 1 MFVRSDFPKPTAVEISNLE.....HTKPSHSVSNSAPNQFRKP 312

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	963	61.3	256	2 F71326	hypothetical prote
2	430.5	27.4	227	2 G71326	hypothetical prote
3	198	12.6	721	2 S29795	hypothetical prote
4	195	12.4	407	1 EDBEO3	immediate-early pr
5	187.5	11.9	2109	2 E89066	protein H05009.1 l
6	187.5	11.9	2109	2 T33247	hypothetical prote
7	187	11.9	630	2 S29796	hypothetical prote
8	185	11.8	1271	2 A45555	glutamate rich pro
9	176	11.2	913	2 T52485	neurofilament prot
10	175	11.1	391	2 C29450	surface antigen Tc
11	174	11.1	450	1 C29450	ubiquitinol-cytocho
12	166.5	10.6	1094	2 S49313	protein kinase - s
13	165.5	10.5	590	2 A40437	glutamic acid-rich
14	162	10.3	1110	2 I51116	NF-180 - sea lamp
15	159	10.1	1881	2 H95076	zinc metalloprotei
16	157	10.0	1621	2 A82255	hypothetical prote
17	156.5	10.0	296	2 A54527	110k antigen - pla
18	153.5	9.8	849	2 S00030	neurofilament trip
19	153	9.7	518	2 G84488	En/Spm-like transp
20	151.5	9.6	1020	1 QFRH0	neurofilament trip
21	151.5	9.6	1076	2 F96831	hypothetical prote
22	151	9.6	845	2 A45669	neurofilament trip
23	150.5	9.6	798	2 T33022	hypothetical prote
24	150	9.5	679	2 S28366	recombination repa
25	148	9.4	1963	2 B98002	IGA-specific metal
26	145.5	9.3	506	2 S47439	I2 protein - tyra
27	145.5	9.3	5170	2 T13348	hypothetical prote
28	145	9.2	644	2 S55395	neurofilament prot
29	145	9.2	837	2 T03761	outer arm dynein t

30	145	9.2	1791	2 T02345	hypothetical prote
31	145	9.2	2004	2 F95133	immunoglobulin A1
32	142.5	9.1	7962	2 I38346	elastic titin - hu
33	141.5	9.0	630	2 T28700	hypothetical prote
34	140.5	8.9	333	2 T10738	hypothetical prote
35	140.5	8.9	544	1 I36911	involucrin L - dou
36	140.5	8.9	706	2 A45930	junctional sarcopl
37	140	8.9	2336	2 A45386	omega-conotoxin-se
38	138	8.8	1566	2 A43607	cell surface anti
39	137.5	8.7	1262	2 T22523	hypothetical prote
40	137	8.7	880	2 D89756	protein T23E7.2b l
41	136.5	8.7	916	2 A27864	neurofilament trip
42	136	8.7	311	2 A48481	antigen C-termina
43	136	8.7	754	2 AC2807	Cmpa family protei
44	136	8.7	754	2 B97586	hypothetical prote
45	136	8.7	784	2 P00009	neurofilament trip

ALIGNMENTS

RESULT 1

F71326
hypothetical protein TP0433 - syphilis spirochete

C/Species: Treponema pallidum subsp. pallidum (syphilis spirochete)

C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004

C/Accession: F71326

R/Frazer, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwi

reton, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uetzerback, T.; McI

they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.

A/Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.

A/Reference number: A71250; PMID:9665876

A/Accession: F71326

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-256 <COL>

A/Cross-references: UNIPROT:083448; GB:AE001220; GB:AE000520; NID:93322705; PIDDN:AA654

A/Experimental source: strain Nichols

C/Genetics:

Query Match 61.3%; Score 963; DB 2; Length 256;
Best Local Similarity 98.5%; Pred. No. 9.1e-51;
Matches 192; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MFVRSDFPKPTAVEISNLEKNAKAQAVTGHAGIPGLVSLAPAAQAOLGIGYQAVRV 60

DB 57 MFVRSDFPKPTAVEISNLEKNAKAQAVTGHAGIPGLVSLAPAAQAOLGIGYQAVRV 116

QY 61 RVRTLTGTVRGGSQTSODGLSLASLPSRVAPAPQADPLSSBPAGHVPVRYDTVI FDDPR 120

DB 117 RVRTLTGTVRGGSQTSODGLSLASLPSRVAPAPQADPLSSBPAGHVPVRYDTVI FDDPR 176

QY 121 LVSPLSREVEDVPKVPASREGEREVEDVPKVPASREGEREVEDVPKVPAS 180

DB 177 LVSPLSREVEDVPKVPASREGEREVEDVPKVPASREGEREVEDVPKVPAS 236

QY 181 EREGEREVEDVPKV 195

DB 237 EREGEREVEDVPKV 251

RESULT 2

G71326
hypothetical protein TP0434 - syphilis spirochete

C/Species: Treponema pallidum subsp. pallidum (syphilis spirochete)

C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004

C/Accession: G71326

R/Frazer, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwi

reton, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uetzerback, T.; McI

they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.

Science 281, 375-388, 1998

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OM protein - protein search, using sw model

Run on: March 16, 2005, 21:13:20 ; Search time 79.1429 Seconds

(without alignments)
2018.738 million cell updates/sec

Title: US-10-017-168-6

Perfect score: 1572

Sequence: 1 MFVRSDFPKNTAVEISNLE.....HTKQSHSVNSAPNQFRKP 312

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1567	99.7	428	Q9ALV6	Q9ALV6 treponema p
2	1480	94.1	432	O51953	O51953 treponema p
3	1479	94.1	548	O93CA4	O93CA4 treponema p
4	1364.5	86.8	393	O93CA3	O93CA3 treponema p
5	1113	70.8	348	O9ALV7	O9ALV7 treponema p
6	963	61.3	256	O83448	O83448 treponema p
7	430.5	27.4	227	O83449	O83449 treponema p
8	345.5	22.0	458	O73NG7	O73NG7 treponema d
9	244.5	15.6	432	O964C9	O964C9 encephalito
10	237.5	15.1	1112	O63G96	O63G96 bacillus ce
11	228.5	14.5	410	O962T4	O962T4 encephalito
12	215	13.7	1167	O7SH84	O7SH84 neurospora
13	211	13.4	466	O6NE60	O6NE60 magnetospir
14	208.5	13.3	1070	O81Y70	O81Y70 bacillus an
15	206	13.1	5458	O9U459	O9U459 plasmodium
16	202.5	12.9	394	O964D0	O964D0 encephalito
17	202.5	12.6	453	O63G96	O63G96 bacillus ce
18	198.5	12.6	248	O9LRH2	O9LRH2 encephalito
19	198	12.6	721	YCF2_OENPI	YCF2_OENPI raphanus sa
20	195	12.4	407	IE68_SHV21	IE68_SHV21 plasmodium
21	190.5	12.1	614	O94674	O94674 plasmodium
22	189.5	12.1	630	O9VC00	O9VC00 brachydanio
23	187.5	11.9	2768	O9VC00	O9VC00 brachydanio
24	187.5	11.9	10578	O81SF5	O81SF5 caenorhabdi
25	187.5	11.9	18519	O81SF6	O81SF6 caenorhabdi
26	187.5	11.9	18534	O81SF7	O81SF7 caenorhabdi
27	187	11.9	630	YCF2_OENVI	YCF2_OENVI raphanus sa
28	186	11.8	982	O6CGV5	O6CGV5 yarrowia v
29	185	11.8	1271	O25860	O25860 plasmodium
30	182	11.6	1108	O9ND10	O9ND10 plasmodium
31	181.5	11.5	1554	O7RMK1	O7RMK1 babesia big

32	180.5	11.5	716	2	Q801T3	Q801T3 xenopus lae
33	180.5	11.5	843	2	O6GLM0	O6GLM0 xenopus lae
34	180.5	11.5	897	2	O13098	O13098 xenopus lae
35	177.5	11.3	1233	2	O81J56	O81J56 plasmodium
36	177	11.3	601	2	O711E3	O711E3 streptococ
37	176	11.2	913	2	O13099	O13099 xenopus lae
38	176	11.2	913	2	O6DCC0	O6DCC0 xenopus lae
39	175.5	11.2	261	2	O9U4B1	O9U4B1 plasmodium
40	175	11.1	391	2	O26892	O26892 trypanosoma
41	174	11.1	450	1	CY1_PANDE	CY1_PANDE paracoccus
42	173	11.0	979	2	O819Y2	O819Y2 plasmodium
43	173	11.0	2191	2	O7RY51	O7RY51 neurospora
44	172	10.9	722	2	O26893	O26893 trypanosoma
45	171.5	10.9	917	2	O61MK4	O61MK4 rattus norv

ALIGNMENTS

RESULT 1

ID	Q9ALV6	PRELIMINARY;	PRT;	428 AA.
AC	Q9ALV6			
DT	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)			
DE	Acidic repeat protein.			
GN	Name=arp; pallidum subsp. endemicum.			
OS	Treponema pallidum subsp. endemicum.			
OC	Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.			
OX	NCBI_TaxID=53436;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Bozma.			
RA	Liu H., Steiner B.;			
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Bozma;			
RA	Liu H., Steiner B.M., Rodas B.;			
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF342807; AK01461.2; -			
SQ	SEQUENCE 428 AA; 46710 MW; B14ED8A074D43933 CRC64;			

Query Match 99.7%; Score 1567; DB 2; Length 428;

Best Local Similarity 99.7%; Pred. No. 8.3e-79; Mismatches 1; Indels 0; Gaps 0;

QY	1	MFVRSDFPKNTAVEISNLEKNKAQAQAVVIGHAGIPGLLVSLAPAAQAGIGVQAVRV	60
DB	1	MFVRSDFPKNTAVEISNLEKNKAQAQAVVIGHAGIPGLLVSLAPAAQAGIGVQAVRV	60
QY	61	RRRTLTGVGGSGTSDGLSLASLPSSRPVAPPAQDPLSSPPAGTTPVETRTVTFDDRR	120
DB	61	RRRTLTGVGGSGTSDGLSLASLPSSRPVAPPAQDPLSSPPAGTTPVETRTVTFDDRR	120
QY	121	LVSPLSREVEDVPKVEPASERGGERVEDVPKVEPASERGGERVEDVPKVEPAS	180
DB	121	LVSPLSREVEDVPKVEPASERGGERVEDVPKVEPASERGGERVEDVPKVEPAS	180
QY	181	EBRGGERVEDVPKVEPASERGGERVEDVPKVEPASERGGERVEDVPKVEPAS	240
DB	181	EBRGGERVEDVPKVEPASERGGERVEDVPKVEPASERGGERVEDVPKVEPAS	240
QY	241	EBRGGERVEDVPKVEPASERGGERVEDVPKVEPASERGGERVEDVPKVEPAS	300
DB	241	EBRGGERVEDVPKVEPASERGGERVEDVPKVEPASERGGERVEDVPKVEPAS	300
QY	301	VNSAPNPFQRP 312	
DB	301	VNSAPNPFQRP 312	

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OM protein - protein search, using sw model

Run on: March 16, 2005, 21:10:15 ; Search time 62.4615 Seconds
(without alignments)

1436.539 Million cell updates/sec

Title: US-10-017-168-4

Perfect score: 1168

Sequence: 1 MFVRSDFPKNTAVETISNLE.....HTKQPSHSVNSAPNQFRKP 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16nc04:*
1: geneseqp18808:*
2: geneseqp19908:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20048:*
8: geneseqp20058:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1168	100.0	232	4 AAB48317	Aab48317 T. pallid
2	1118	95.7	312	4 AAB48318	Aab48318 T. pallid
3	1048	89.7	432	4 AAB48316	Aab48316 T. pallid
4	138.5	11.9	1018	2 AAB98747	Aab98747 P. vivax
5	138.5	11.9	1018	2 AAB97039	Aab97039 A. secreta
6	138.5	11.9	1018	2 AAG65528	Aag65528 Plasmodiu
7	138.5	11.9	1018	2 ADJ95471	Adj95471 Plasmodiu
8	137	11.7	25	4 AAB48324	Aab48324 T. pallid
9	124.5	10.7	2109	8 ADN23693	Adn23693 Bacterial
10	124.5	10.7	19938	6 ABP76681	Abp76681 Streptomy
11	124	10.6	25	4 AAB48323	Aab48323 T. pallid
12	122	10.4	676	4 ABG11370	Abg11370 Novel hum
13	122	10.4	676	4 ABG29412	Abg29412 Novel hum
14	122	10.4	676	4 ABG11395	Abg11395 Novel hum
15	121	10.4	26	4 AAB48326	Aab48326 T. pallid
16	121	10.4	2768	4 ABB68397	Abb68397 Drosophila
17	119.5	10.2	1791	6 ABO52986	Abos2986 Human put
18	119.5	10.2	2263	7 ADJ70425	Adj70425 Human hea
19	119.5	10.2	2296	8 ADN60280	Adn60280 Human sp1
20	119.5	10.2	2752	8 ADN60278	Adn60278 Human ser
21	119.5	10.2	2752	8 ADP24102	Adp24102 PFO polyp
22	117.5	10.1	540	6 ABR44276	Abrr44276 Novel hum
23	117	10.0	278	2 AAW5109	Aaw5109 Streptoco
24	117	10.0	278	5 ABP54603	Abp54603 S. pneumo
25	117	10.0	278	7 ADC45175	Adc45175 S. pneumo

26	117	10.0	571	2 AAW55064	Aaw55064 Streptoco
27	117	10.0	571	5 ABP54558	Abp54558 S. pneumo
28	117	10.0	571	7 ADC45085	Adc45085 S. pneumo
29	117	10.0	1963	6 ABU46054	Abu46054 Protein e
30	117	10.0	1965	2 AAW69165	Aaw69165 Streptoco
31	117	10.0	1965	8 ADK47314	Adk47314 Streptoco
32	117	10.0	1972	8 ADR94616	Adr94616 Novel S.
33	117	10.0	2004	6 ABU01577	Abu01577 S. pneumo
34	117	10.0	2004	6 ADM92167	Adm92167 S. pneumo
35	116	9.9	258	2 AAW55107	Aaw55107 Streptoco
36	116	9.9	258	5 ABP54601	Abp54601 S. pneumo
37	116	9.9	258	7 ADC45171	Adc45171 S. pneumo
38	116	9.9	552	7 ADC31182	Adc31182 Human nov
39	116	9.9	565	2 AAW61247	Aaw61247 Streptoco
40	116	9.9	565	5 ABP54665	Abp54665 S. pneumo
41	116	9.9	565	7 ADC45299	Adc45299 S. pneumo
42	116	9.9	1881	3 AAY44506	Aay44506 Streptoco
43	116	9.9	1881	6 ABU01047	Abu01047 S. pneumo
44	116	9.9	1881	8 ADM92119	Adm92119 S. pneumo
45	113	9.7	456	4 ABB58301	Abb58301 Drosophila

ALIGNMENTS

RESULT 1	
AAB48317	
ID	AAB48317 standard; protein; 232 AA.
XX	
AC	AAB48317;
XX	
DT	11-SEP-2003 (revised)
DT	20-APR-2001 (first entry)
XX	
DE	T. pallidum ssp. pertenue (CDC-2) acidic repeat protein (arp).
XX	
KW	Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis; yaws; bejel.
XX	
OS	Treponema pallidum; ssp. pertenue.
PN	WO200077486-A2.
PD	
PD	21-DEC-2000.
PF	14-JUN-2000; 2000WO-US016425.
XX	
PR	14-JUN-1999; 99US-0138981P.
XX	
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.
XX	
PI	Liu H, Steiner B, Rhodes B;
XX	
DR	WPI; 2001-080711/09.
XX	
DR	N-PSDB; AAC84648.
XX	
PT	Detecting Treponema pallidum in blood, saliva, etc., by detecting formation of a complex between immunogenic peptides of acidic repeat protein of the bacterium and an antibody present in the biological sample.
PT	
XX	
PS	Claim 15; Fig 8; 73pp; English.
XX	
CC	The invention relates to a method of detecting presence of Treponema pallidum (TP), anti-treponemal antibodies (Abs), or both in a biological sample that involves contacting an acidic repeat protein (arp), or one or more isolated immunogenic TP peptides of arp with an Ab containing biological sample and then detecting the formation of a complex between immunogenic peptides and Ab. The presence of the complex indicates the presence of TP. The method is thus useful for diagnosing syphilis, yaws, and bejel diseases. The immunogenic peptides or the Abs raised against arp, as part of an immunogenic composition, are useful for inducing a protective immune response against syphilis, yaws or bejel caused by TP.

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OM protein - protein search, using sw model

Run on: March 16, 2005, 21:13:20 ; Search time 58.8498 Seconds
(without alignments)
2018.738 Million cell updates/sec

Title: US-10-017-168-4

Perfect score: 1168

Sequence: 1 MFVRSMDPFPKNTAVEISNLE.....HTKQPSHSVSNAPNQFRKP 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Uniprot_03:*
2: uniprot_sprot:*
3: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1163	99.6	348	2	Q9ALV7
2	1130.5	96.8	393	2	Q9JCA3
3	1113	95.3	428	2	Q9ALV6
4	1048	87.7	432	2	Q9ALV6
5	1043	88.3	548	2	Q9JCA4
6	963	82.4	256	2	Q9JCA4
7	429	36.7	227	2	Q9JCA4
8	286	24.5	458	2	Q9JCA4
9	162	13.9	410	2	Q9JCA4
10	160	13.7	432	2	Q9JCA4
11	152.5	13.1	466	2	Q9JCA4
12	147	12.6	394	2	Q9JCA4
13	147	12.6	453	1	PTPL_BNCHB
14	146.5	12.5	1167	2	Q9JCA4
15	144.5	12.4	1070	2	Q9JCA4
16	144	12.3	1112	2	Q9JCA4
17	133.5	11.4	891	2	Q9JCA4
18	129	11.0	675	2	Q9JCA4
19	126.5	10.8	614	2	Q9JCA4
20	125.5	10.7	519	2	Q9JCA4
21	125.5	10.7	915	2	Q9JCA4
22	124.5	10.7	10578	2	Q9JCA4
23	124.5	10.7	18519	2	Q9JCA4
24	124.5	10.7	18534	2	Q9JCA4
25	123.5	10.6	796	2	Q9JCA4
26	122	10.4	1942	2	Q9JCA4
27	121.5	10.4	690	2	Q9JCA4
28	121	10.4	687	2	Q9JCA4
29	121	10.4	2768	2	Q9JCA4
30	120	10.3	1754	2	Q9JCA4
31	120	10.3	2607	2	Q9JCA4

32	119.5	10.2	802	2	Q9UQ37	Q9UQ37	homo sapien
33	119.5	10.2	1783	2	Q15038	Q15038	homo sapien
34	119.5	10.2	1791	2	Q60382	Q60382	homo sapien
35	119.5	10.2	2296	2	Q9UQ48	Q9UQ48	homo sapien
36	119.5	10.2	2752	2	Q9UQ35	Q9UQ35	homo sapien
37	119.5	10.2	1010	2	Q7TT35	Q7TT35	mus sapien
38	119	10.2	1012	1	PHCI_MOUSE	PHCI_MOUSE	mus sapien
39	118	10.1	218	2	Q96NZO	Q96NZO	mus sapien
40	118	10.1	491	2	Q6LS04	Q6LS04	homo sapien
41	118	10.1	630	1	YCF2_OENV1	YCF2_OENV1	homo sapien
42	118	10.1	982	2	Q6CGV5	Q6CGV5	homo sapien
43	117.5	10.1	1394	1	CNG4_BOVIN	CNG4_BOVIN	homo sapien
44	117	10.0	1081	2	Q7SBY5	Q7SBY5	homo sapien
45	117	10.0	1621	2	Q9KTA5	Q9KTA5	homo sapien

ALIGNMENTS

RESULT 1	Q9ALV7	PRELIMINARY;	PRT;	348 AA.
ID	Q9ALV7			
AC	Q9ALV7			
DT	01-JUN-2001 (Tremblrel. 17, Created)			
DT	01-DEC-2001 (Tremblrel. 19, Last sequence update)			
DT	01-OCT-2002 (Tremblrel. 22, Last annotation update)			
DE	Acidic repeat protein.			
CN	Name=arp;			
OS	Treponema pallidum (subsp. pertenue) (Yaws treponema).			
OC	Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.			
OX	NCBI_TaxID=168;			
ON	(1)			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CDC2;			
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CDC2;			
RA	Liu H., Steiner B.M., Rodas B.;			
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF342806; AA01460.2;			
SQ	SEQUENCE 348 AA; 37936 MW; E4A446BD2344592 CRC64;			
Query Match	99.6%; Score 1163; DB 2; Length 348;			
Best Local Similarity	99.6%; Pred. No. 1.1e-66;			
Matches	231; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
QY	1 MFVRSMDPFPKNTAVEISNLEKNAKQAVIGHAGIPGLVSLAPAAAGIGYQAVRV			60
DB	1 MFVRSMDPFPKNTAVEISNLEKNAKQAVIGHAGIPGLVSLAPAAAGIGYQAVRV			60
QY	61 RVRLGTVRGSGSQTSDGLSLASIPSRVAPAPAPQDRDLSSPPAGHTVPEYRDTVIFDDPR			120
DB	61 RVRLGTVRGSGSQTSDGLSLASIPSRVAPAPAPQDRDLSSPPAGHTVPEYRDTVIFDDPR			120
QY	121 LVSPLSREVDVPPVPPASEREGREVDVPPVPPASEREGREVDVPPVPPAS			180
DB	121 LVSPLSREVDVPPVPPASEREGREVDVPPVPPASEREGREVDVPPVPPAS			180
QY	181 EREGREVDVPPVPPASEREGREVDVPPVPPASEREGREVDVPPVPPAS			232
DB	181 EREGREVDVPPVPPASEREGREVDVPPVPPASEREGREVDVPPVPPAS			232
RESULT 2	Q9JCA3	PRELIMINARY;	PRT;	393 AA.
ID	Q9JCA3			
AC	Q9JCA3			
DT	01-DEC-2001 (Tremblrel. 19, Created)			
DT	01-DEC-2001 (Tremblrel. 19, Last sequence update)			
DT	01-OCT-2002 (Tremblrel. 22, Last annotation update)			
DE	Acidic repeat protein.			

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OM protein - protein search, using sw model

Run on: March 16, 2005, 21:14:51 ; Search time 13.1722 Seconds

(without alignments)
1694.657 Million cell updates/sec

Title: US-10-017-168-4

Sequence: 1 MFVRSDFPPKNTAVEISNLE.....HTKQPSHSVNSAPNQFRKP 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: PIR 79:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	963	82.4	256	F71326	hypothetical prote
2	429	36.7	227	G71326	hypothetical prote
3	124.5	10.7	2109	E89066	protein H05009.1
4	124.5	10.7	2109	T33247	hypothetical prote
5	119.5	10.2	1791	T02345	hypothetical prote
6	119	10.2	1012	I53172	RAE-28 - mouse
7	118	10.1	630	S29796	hypothetical prote
8	117.5	10.1	590	A40437	glutamic acid-rich
9	117	10.0	1621	A82255	hypothetical prote
10	117	10.0	1963	B98002	IGF-specific metal
11	117	10.0	2004	P85133	immunoglobulin A1
12	116	9.9	1881	H95076	zinc metalloprotei
13	114	9.8	407	EDBEQ3	immediate-early pr
14	114	9.8	450	C29413	ubiquitinol-cytochro
15	113.5	9.7	1384	T26566	hypothetical prote
16	113.5	9.7	1611	T38236	hypothetical prote
17	113	9.7	1078	T42712	myelin transcripti
18	112	9.6	880	D89756	protein T23E7.2b
19	111.5	9.5	798	T33022	hypothetical prote
20	111	9.5	391	S27850	surface antigen Tc
21	110.5	9.5	184	S48035	hypothetical prote
22	109.5	9.4	630	T28700	hypothetical prote
23	109	9.3	721	S29795	hypothetical prote
24	108.5	9.3	554	TW0094	neurofilament prot
25	108.5	9.3	585	T47364	hypothetical prote
26	108	9.2	364	S44897	ZK136.2 protein -
27	108	9.2	1566	A43607	cell surface antig
28	107.5	9.2	1390	T14004	trfA protein - sli
29	107.5	9.2	2440	S39162	transcription coac

30	106.5	9.1	1094	2	S49313	protein kinase - s
31	106	9.1	459	2	I38013	p54/S8N - human
32	106	9.1	543	1	QFMSL	neurofilament trip
33	105.5	9.0	583	2	AG2832	cell division prot
34	105.5	9.0	583	2	C97610	cell division prot
35	105.5	9.0	2722	2	T20532	hypothetical prote
36	105.5	9.0	2738	2	E88320	protein F07A11.6
37	105	9.0	789	2	E84514	hypothetical prote
38	104.5	8.9	548	1	QFPGI	neurofilament trip
39	104	8.9	400	2	D82572	neurofilament prot
40	103.5	8.9	913	2	T52485	neurofilament prot
41	103	8.8	542	2	T29707	hypothetical prote
42	102	8.7	465	2	S46759	hypothetical prote
43	102	8.7	761	1	TVCHM	transforming prote
44	101.5	8.7	544	2	S07144	neurofilament trip
45	101.5	8.7	655	2	T28885	hypothetical prote

ALIGNMENTS

RESULT 1
F71326
hypothetical protein TP0433 - syphilis spirochete
C/Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C/Accession: F71326
R/Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwlr
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uetzerback, T.; McDC
Science 281, 375-388, 1998
A/Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A/Reference number: A71250; MUID:9832770; PMID:9665876
A/Accession: F71326
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-256 <COL>
A/Cross-references: UNIPROT:O83448; GB:AE001220; GB:AE000520; NID:G3322705; PIDN:AAC6542
A/Experimental source: strain Nichols
C/Genetics:
A/Gene: TP0433

Query Match 82.4%; Score 963; DB 2; Length 256;
Best Local Similarly 98.5%; Pred. No. 3.6e-57;
Matches 192; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1	MFVRSDFPPKNTAVEISNLEKNAKAQAVVIGHAGIPGLVSLAPAAAGIGYQAVRV	60
Db	57	MFVRSDFPPKNTAVEISNLEKNAKAQAVVIGHAGIPGLVSLAPAAAGIGYQAVRV	116
Qy	61	RVRTLTGVRGSGQTSODGLSLASLPKRVPAQRPPLSPAGHVTPEYRDVTPDDPR	120
Db	117	RVRTLTGVRGSGQTSODGLSLASLPKRVPAQRPPLSPAGHVTPEYRDVTPDDPR	176
Qy	121	LVSPFLREVEDVPRVVEPASEREGEREVDVPRVVEPASEREGEREVDVPRVVEPAS	180
Db	177	LVSPFLREVEDVPRVVEPASEREGEREVDVPRVVEPASEREGEREVDVPRVVEPAS	236
Qy	181	EREGEREVEDVPRV 195	
Db	237	EREGEREVEDVPRV 251	

RESULT 2
G71326
hypothetical protein TP0434 - syphilis spirochete
C/Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C/Accession: G71326
R/Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwlr
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uetzerback, T.; McDC
Science 281, 375-388, 1998